

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(ii) TITLE OF INVENTION: Novel CREBa Isoform

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MARshall, O'Toole, Gerstein, Murray & Borun
- (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower
- (C) CITY: Chicago
- (D) STATE: Illinois
- (E) COUNTRY: USA
- (F) ZIP: 60606

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: Januray 12, 1998
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Williams Jr., Joseph A.
- (B) REGISTRATION NUMBER: 38,659
- (C) REFERENCE/DOCKET NUMBER: 27866/33469

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 312-474-6300
- (B) TELEFAX: 312-474-0448

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 304..1866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG ACTTTCTTGG GATGAGCGCT GCCTTTTGG CTTCCTTTG GATGCACAGC 60  
CCGATTTAAC CCCTGCACCT TCCGCCGAT CCCAGCAGGC TTGTCTCCC CGGGGAGTCA 120  
CAGATTTCCG AGGACAAGGG TCGCGTAGCC TTCGGCAGGG CTCTCCGAG TTCTGCTCC 180  
AGTGCATAAG TTCCACGGCGC GCACACGCCA AGTACACGGG GAGAACGTC TCACCGGCC 240  
GCGGCGGCTC TGCGCGGTCC CCTCCTGCCT CAGCATCCTC GGGCCTGCGC GGCGCCCACC 300  
GCC ATG GAG GTG CTG GAG AGC GGG GAG CAG AGC GTC CTG CAG TGG GAC 348  
Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp  
1 5 10 15  
CGC AAG CTG AGC GAG CTG TCA GAG CCC GGA GAG ACT GAG GCC CTC ATG 396  
Arg Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met  
20 25 30  
TAC CAC ACG CAC TTC TCG GAG CTC CTA GAC GAG TTT TCC CAG AAC GTC 444  
Tyr His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val  
35 40 45  
CTG GGT CAG CTC CTG AGT GAC CCT TTC CTC TCA GAG AAG AGC GAG TCA 492  
Leu Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser  
50 55 60  
ATG GAG GTG GAG CCA TCT CCA ACA TCA CCA GCG CCT CTC ATC CAG GCT 540  
Met Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala  
65 70 75  
GAA CAC AGC TAC TCT CTG AGC GAG GAG CCC CGG ACT CAG TCA CCA TTT 588  
Glu His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe  
80 85 90 95  
ACC CAT GCG GCT ACC AGC GAC AGC TTC AAT GAC GAG GAG GTG GAG AGT 636  
Thr His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser  
100 105 110  
GAA AAA TGG TAC CTG TCT ACA GAG TTT CCT TCA GCT ACC ATC AAG AAA 684  
Glu Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys  
115 120 125  
GAG CCA ATC ACA GAG GAG CAG CCC CCG GGA CTT GTC CCT TCT GTC ACT 732  
Glu Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr  
130 135 140  
CTG ACC ATC ACA GCC ATT TCC ACT CCT TTT GAA AAA GAA GAG TCC CCT 780  
Leu Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro  
145 150 155  
CTG GAT ATG AAT GCT GGG GGG GAC TCC TCA TGC CAG ACG CTT ATT CCT 828

09884566  
061904

Leu Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro	160	165	170	175	
AAG ATT AAG CTG GAG CCC CAC GAA GTG GAT CAG TTC TTA AAC TTC TCC					876
Lys Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser	180	185	190		
CCG AAA GAA GCC TCC GTG GAT CAA CTG CAC TTA CCA CCA ACA CCA CCC					924
Pro Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro	195	200	205		
AGT AGT CAC AGC AGT GAC TCT GAG GGC AGC TTG AGC CCC AAC CCA CGC					972
Ser Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg	210	215	220		
CTG CAT CCC TTC AGC CTG TCT CAG GCC CAC AGC CCT GTC AGA GCC ATG					1020
Leu His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met	225	230	235		
CCC CGG GGC CCC TCT GCC TTG TCC ACA TCT CCT CTC CTC ACA GCT CCA					1068
Pro Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro	240	245	250	255	
CAT AAG CTG CAG GGA TCG GGC CCC CTG GTC CTG ACA GAA GAG GAG AAG					1116
His Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys	260	265	270		
AGG ACC CTG GTT GCC GAG GGC TAT CCC ATT CCC ACC AAG CTG CCT CTG					1164
Arg Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu	275	280	285		
ACA AAA TCT GAG GAG AAG GCC CTG AAG AAA ATC CGG AGA AAG ATC AAG					1212
Thr Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys	290	295	300		
AAT AAG ATT TCT GCC CAA GAA AGC AGG AGA AAG AAG AAA GAA TAC ATG					1260
Asn Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Glu Tyr Met	305	310	315		
GAC AGC CTG GAG AAA AAA GTG GAG TCT TGT TCA ACT GAG AAC TTG GAG					1308
Asp Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu	320	325	330	335	
CTT CGG AAG AAG GTG GAG GTG CTG GAG AAC ACC AAT AGG ACT CTC CTT					1356
Leu Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu	340	345	350		
CAG CAA CTT CAG AAG CTT CAG ACT TTG GTG ATG GGG AAG GTC TCT CGA					1404
Gln Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg	355	360	365		
ACC TGC AAG TTA GCT GGC ACA CAG ACT GGC ACC TGC CTC ATG GTC GTT					1452
Thr Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val	370	375	380		

GTG CTT TGC TTT GCT GTT GCA TTT GGA AGC TTC TTT CAA GGC TAT GGG Val Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly 385 390 395	1500
CCT TAT CCT TCT GCC ACC AAG ATG GCT CTG CCC AGC CAG CAT CCT CTG Pro Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu 400 405 410 415	1548
TCA GAG CCA TAC ACA GCC TCC GTG GTG AGA TCC AGG AAC CTG CTA ATC Ser Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile 420 425 430	1596
TAT GAG GAA CAC GCT CCC CTG GAA GAG TCG TCG AGC CCA GCC TCA ACC Tyr Glu Glu His Ala Pro Leu Glu Ser Ser Ser Pro Ala Ser Thr 435 440 445	1644
GGG GAG CTG GGG GGC TGG GAC AGA GGC TCC TCT CTG CTC AGG GCA TCG Gly Glu Leu Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser 450 455 460	1692
TCG GGG CTT GAG GCC CTG CCA GAG GTG GAT CTT CCC CAT TTC CTT ATC Ser Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile 465 470 475	1740
TCC AAT GAG ACG AGC TTG GAG AAG TCA GTA CTG TTG GAG CTT CAG CAG Ser Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln 480 485 490 495	1788
CAC CTG GTC AGC AGC AAA CTG GAA GGG AAC GAA ACA CTC AAG GTT GTA His Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val 500 505 510	1836
GAG CTG GAG AGG AGA GTG AAC GCC ACC TTC TGAGGAGAGC TCCACCCCTCC Glu Leu Glu Arg Arg Val Asn Ala Thr Phe 515 520	1886
TCTTCTCCTA ACTCCATCTG ATCGTCCTTT CAGTTCCCCC TTCACCACTG GATCTCGAGG AGGAGATGGC TAGTGTACG GCTCGAGACA GGAGGCCAGC CCAGGGGTT CTGCTTATGT	1946
GTCCCCGTGG CTCTCCACAA AAGGGAGCTA GCACCTCTCC ATCCCTTCT CTTACTGCCA	2006
TTGGAAATTA TTTTAGGGCT GAGATAGGGG TGGAACGAGC AGGCTTGTGTT CCACCAATAG	2066
TGCCAAGAAG ACAC TGCTG ATTCTCCCC GGGAGGGAGTG ACTCCTCTGA AGAAGACATG	2126
ACTCATGTTA AGTTGAGACC CCAGACTCTA GCCACACACA TGCCACAGAC ATGCCAGGGA	2186
GTGGCAAAGC ACTGACTCCT GAGCTCCCTT CCTCACTAGG ACTCCAGTGT GACCCTGCAC	2246
TGAGAGGACC AAAGCGTCAT TGCAGTCTTC TCTCCACCC GTACCCCGGA GTCCTGATTG	2306
GATGTCTGCA GAGGCAGATG GGGCTCCAC CATATTTCA GGCGCAAGT GCAATTCCCTG	2366
	2426

AAGGCATCAG GCTCTTCTCT CCCAGGCTCT CCTGCCACT GTGTTGTTG TAGGACACCC 2486  
CCACACCCAC TCATACACAG CCTGCATCTC CACAGGACAA TAGCTCTGTC TCCCTGGCCT 2546  
CCCCTCCCCA TTTGTAAATA GTATTTATTA GCTTGCTCAA GCTCCCAGCT GGCCATAGTG 2606  
AAAAGATTTC CCCTTCAAC CAGCAAAGTC TTCTGTTGGC CTTTGGAAACA GGAGAGTCCC 2666  
CGGAATCTAG GACCCTAGTC TTTGTACTTG ATGCCTTGT TCCCCCCTTT TCTTCTTTAA 2726  
AATTGGGGAC CTATAACATC ATCGCTGTTG CGGAATCCAC TTAGGCATGT GTCCCCGTAT 2786  
GGATGAATAC ATGGGAATGG TGGATACTGT CTTCTGACTC AGGCTCTAGG CTCCATGGCT 2846  
TCCTCTCTCT GGTCTGCCA CACAGAAGGA AAGCCCTGTC CAGGATAATG AGCGTTGCTG 2906  
ACACCCCTTGC TAGCTTGTCC TGCCTACCTG CTTACCCCCAC TCCCTCACCT TCCTCCTTCC 2966  
CTTCTGCCCT CCATCCACCT GCCTTAACTA ATTGGGGCTG GAGTTGGTCA TTTTTTGTAC 3026  
ACCCACAGTG GTACCTTTA CAGTCAGGTT TGGATACTTT GCAGCTCATC CAAAGAGACA 3086  
TAACTAAACC CTAAACTCTT TTTTGTTGT TGTTGTTGT GTTTTTTTT TTTATGATTA 3146  
AAAAAGTAAAA ATTGTAGTTT AAAAAAAA AAAAAAAACT CGAG 3190

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg  
1 5 10 15

Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr  
20 25 30

His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu  
35 40 45

Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met  
50 55 60

Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu  
65 70 75 80

His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr

0200766 061901

85

90

95

His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser Glu  
100 105 110

Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys Glu  
115 120 125

Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr Leu  
130 135 140

Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro Leu  
145 150 155 160

Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro Lys  
165 170 175

Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro  
180 185 190

Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro Ser  
195 200 205

Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg Leu  
210 215 220

His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met Pro  
225 230 235 240

Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro His  
245 250 255

Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys Arg  
260 265 270

Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr  
275 280 285

Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn  
290 295 300

Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Glu Tyr Met Asp  
305 310 315 320

Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu  
325 330 335

Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu Gln  
340 345 350

Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg Thr  
355 360 365

Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val Val

370                    375                    380

Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro  
385                    390                    395                    400

Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser  
405                    410                    415

Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr  
420                    425                    430

Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly  
435                    440                    445

Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser  
450                    455                    460

Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser  
465                    470                    475                    480

Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His  
485                    490                    495

Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu  
500                    505                    510

Leu Glu Arg Arg Val Asn Ala Thr Phe  
515                    520

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGATCCT AATGGAGCTG AGAGTCGGG

29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCGGATCCG CTCATCGGTG CACGACAGA

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ACAGCTCCAC ATAAGCTGC

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAATTCGCT CAAGGAGAGT CCTATTGG

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGGTCAGTT CAGCGGATCC TGTGNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	60
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	120
NNNNNNNNNG AGGCGAATTC AGTGCAACTG CAGC	154

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTCAGTT CAGCGGATCC TGTG	25
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGCAGTTG CACTGAATTC GCCTC	25
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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATCGGGCC GCCGAGATCT CATATGGAGC TGAGAGTC

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